

OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 NCBI_TAXID=1773;
 [1] SEQUENCE FROM N.A.

RP STRAIN-H37RV;
 RX MEDLINE-98295987; PubMed-9631230;
 RX Cole S.T., Broich R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Elgelmier K., Gas S., Barry C.R. III., Tekala P., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., McLean J., Moulis S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Krogh A., Quail M.A., Rajandream M.A., Rogers J., Oliver S., Osborne J., Sulston J.E., Taylor K., Whitehead S., Squires S., Squares R., Utterback T., Waddman J., Khouri H., Gill J., Mikula A., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."; RT Nature 393:537-544(1998).
 [2] RN SEQUENCE FROM N.A.
 RP STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwin M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Onyamwaya L.A., Ernolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Waddman J., Khouri H., Gill J., Mikula A., Bishai W.; "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains"; RT submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO MLEPRAE MU2443.

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 CC -1- SIMILARITY: TO MLEPRAE MU2443.

RC STRAIN-MAFF303099; PubMed-11214968;
 RX RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idezawa K., Ishikawa A., Kawashima K., Kimura T., RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuo A., RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpoo S., Sugimoto M., RT Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti."; RT Mesorhizobium loti.; RL DNA Res. 7:331-338(2000).
 CC -1- FUNCTION: Bidirectionally degrades single-stranded DNA into large acid-insoluble oligonucleotides, which are then degraded further into small acid soluble oligonucleotides (BY similarity).
 CC -1- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'- or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
 CC -1- SUBUNIT: Heterooligomer composed of large and small subunits (BY similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (BY similarity).
 CC -1- SIMILARITY: BELONGS TO THE XSE4 FAMILY.
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 CC -1- SIMILARITY: BELONGS TO THE XSE4 FAMILY.
 CC DR EMBL; AP003010; BAB53097.1; -.
 CC DR HAMAP; MF_00378; -1.
 CC DR InterPro; IPR003753; Exonuc_VII_L.
 CC DR InterPro; IPR004365; tRNA_antii.
 CC DR Pfam; PF02601; Exonuc_VII_L; 1.
 CC DR Pfam; PF01336; tRNA_antii; 1.
 CC DR TIGR00237; XSE4; 1.
 CC DR TIGR00237; XSE4; 1.
 CC KW Hydrolase; Nuclease; Exonuclease; Complete proteome.
 CC SQ SEQUENCE 521 AA; 56317 MW; 6FDDE75D1A2DF085 CRC64;
 CC DR Query Match 43.8%; Score 7; DB 1; Length 521;
 CC DR Best Local Similarity 100.0%; Pred. No. 25;
 CC DR Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC DR QY 4 AARRAA 10
 CC DR 111111
 CC DR 306 AARRAR 312
 CC DR RESULT 10
 CC US26-HCMVVA STANDARD; PRT; 603 AA.
 CC ID US26-HCMVVA
 CC AC P09599;
 CC DT 01-MAR-1989 (Rel. 10, Created)
 CC DT 01-MAR-1989 (Rel. 10, Last sequence update)
 CC DT 01-FEB-1991 (Rel. 17, Last annotation update)
 CC DE Hypothetical protein HHLF5.
 CC GN US26.
 CC OS Human cytomegalovirus (strain AD169).
 CC OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC OC Betaherpesvirinae; Cytomegalovirus.
 CC NCBITaxID=10360;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC MEDLINE-#1169717; PubMed-3031311;
 CC RX Weston K., Barrell B.G.;
 CC RT "sequence of the short unique region, short repeats, and part of the long repeats of human cytomegalovirus.";
 CC RL J. Mol. Biol. 192:177-208(1986).
 CC [2]
 CC RN COMPLETE GENOME;
 CC RX MEDLINE-#0263039; PubMed-2161319;
 CC AC Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., RA Horsnell T., Hutchison C.A., III, Kouzrides T., Martignetti J.A., RA Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
 CC RN SEQUENCE FROM N.A.
 CC [1]

DR	PROSITE; PS00599; AA_TRANSFER_CLASS_2; 1;
KW	Heme biosynthesis; Transferase; Acyltransferase; Mitochondrion.
KW	Pyridoxal phosphate.
FT	Transit Peptide; Pyridoxal phosphate.
TRANSIT	1 ?
CHAIN	1 ?
FT	621 5-AMINOLEVULINIC ACID SYNTHASE.
FT	362 PYRIDOXAL PHOSPHATE (PROBABLE).
FT	621 AA; 67426 MW; A335C3266FAE1AA3 CRC64;
SEQUENCE	
Query Match	43.8%; Score 7; DB 1; Length 621;
Best Local Similarity	100.0%; Pred. No. 28;
Matches	7; Conservative 0; Mismatches 0; Indels 0;
Qy	4 AARAAAR 10
Db	54 AARAAAR 60
RESULT 12	
UL47_HSVBP	STANDARD; PRT; 742 AA.
ID	UL47_HSVBP
AC	P30021;
DT	01-APR-1993 (Rel. 25, Created)
DT	01-APR-1993 (Rel. 25, Last sequence update)
DT	01-JUN-1994 (Rel. 29, Last annotation update)
DE	80.7 kDa alpha trans-inducing protein (VP8 tegument protein) (VP8 protein) (107 kDa protein).
GN	Bovine herpesvirus type 1 (strain P8-2).
OS	Viruses; dsDNA viruses; no RNA stage; Herpesviridae; OC
OC	Alphaherpesvirinae; Varicellovirus.
OX	NCBITAXID=15324;
RN	
RP	SEQUENCE FROM N.A. MEDLINE-9211550; PubMed=1662698;
RX	
RA	Carpenter D.E.; Misra V.;
RA	"The most abundant protein in bovine herpes 1 virions is a homolog of herpes simplex virus type 1 UL47.";
RT	"The most abundant protein in bovine herpes 1 virions is a homolog of herpes simplex virus type 1 UL47.";
RT	"The most abundant protein in bovine herpes 1 virions is a homolog of herpes simplex virus type 1 UL47.";
RL	J. Gen. Virol. 72:3077-3084 (1991).
CC	-1- FUNCTION: MODULATOR OF ALPHA-TIF (VMW65 PHOSPHOPROTEIN) T1- ACTIVATION. UL47 MAY HAVE KINASE ACTIVITY.
CC	-1- SUBCELLULAR LOCATION: MAJOR TEGUMENT PROTEIN OF THE VIRION.
CC	-1- DEVELOPMENTAL STAGE: EXPRESSED IN THE LATER STAGES OF INFECTION.
CC	-1- PTM: PHOSPHORYLATION.
CC	-1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 AND VZV-1.
CC	-----
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CC	-----
CC	DR D10327; BAA01170.1; -.
CC	DR EMBL: 211610; CAA7683.1; -.
CC	DR PIR: J01435; TNBEB1.
CC	DR InterPro: IPR005039; <i>Herpes_UL47</i> .
CC	DR Pfam: PF03362; <i>Herpes_UL47</i> ; 1.
CC	RW Transcription regulation; trans-acting factor; Structural protein.
CC	KW Late protein; Phosphorylation.
CC	SEQUENCE 742 AA; 80744 MW;
CC	8557979D8C2C953C89 CRC64;
CC	-----
CC	Query Match 43.8%; Score 7; DB 1; Length 742;
CC	Best Local Similarity 100.0%; Pred. No. 33;
CC	Matches 7; Conservative 0; Mismatches 0; Indels 0;
Qy	4 AARAAAR 10
Db	376 AARAAAR 382
RESULT 13	

METL_CAUCA STANDARD; PRT; 777 AA.
ID METL_CAUCA
AC Q9AWV1; 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 5-methyltetrahydropteroylglutamate--homocysteine methyltransferase
DE (BC_2.1.14) (Methionine synthase, vitamin-B12 independent isozyme)
DE (Cobalamin-independent methionine synthase).
GN METE OR CC0482.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN PRODENCE FROM N.A.
RP STRAIN=ATCC 19089 / CB15;
RC MEDLINE=21173698; PubMed=11259647;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephanus C., Phadke N.D., Ely B.,
RA Daboy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smits J., Craven M.B., Khouari H., Shetty J., Berry K.,
RA Utterback T., Tran K., Wolf A., Yamamoto J., Ermolaeva M., White O.,
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).
CC -I- FUNCTION: Catalyzes the transfer of a methyl group from 5'-
CC methyldihydrofolate to homocysteine resulting in methionine
CC formation (By similarity).
CC -I- CATALYTIC ACTIVITY: 5-methyltetrahydropteroyltri-L-glutamate + L-
CC homocysteine -> tetrahydropteroyl-L-glutamate + L-methionine.
CC -I- COFACTOR: Zinc; binds one per subunit (By similarity).
CC -I- PATHWAY: Terminal step in the de novo biosynthesis of methionine.
CC -I- SIMILARITY: Belongs to the 'vitamin-B12 independent methionine
CC synthase family.'.

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CC DR AE005721; AAR22469; 1; -.
DR PIR; A87309; A87309.
DR TIGR; CC0482; -.
DR HAMAP; MF_00172; -; 1.
DR InterPro; IPR002629; Methionine_synt.
DR InterPro; IPR006276; Met_syN_B12ind.
DR Pfam; PF01717; Methionine_synt_1.
DR ProDom; PD004692; Methionine_synt_2.
DR TIGRFAMs; TIGR01371; met_syN_B12ind; 1.
KW Transferase; Methionine transferase; Methionine biosynthesis; Zinc; Repeat; Complete proteome.
KW METAL 665. 665. ZINC (BY SIMILARITY).
FT METAL 667. 667. ZINC (BY SIMILARITY).
FT METAL 750. 750. ZINC (BY SIMILARITY).
SQ SEQUENCE 777 AA; 84380 MW; 1C4DSFD/B80A60F3 CRC64;
Query Match 43.8%; **Score** 7; **DB** 1; **Length** 777;
Best Local Similarity 100.0%; **Pred.** No. 34; **Indels** 0; **Gaps** 0; **Matches** 7; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 8 AARRARA 14
Db 770 AARRARA 776

Query Match 43.8%; **Score** 7; **DB** 1; **Length** 913;
Best Local Similarity 100.0%; **Pred.** No. 39; **Matches** 7; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Qy 7 AAARRR 13
Db 495 AAARR 501

RESULT 14
VGLB_PRVIF
ID VGLB_PRVIF

STANDARD;
PRT; 913 AA.

RESULT 15

VP14_EBV STANDARD; PRT: 1318 AA.

ID VP14_EBV
AC P03175;
DR 21-JUN-1986 (Rel. 01, Created)
DR 21-JUN-1986 (Rel. 01, Last sequence update)
DR 01-APR-1993 (Rel. 25, Last annotation update)
DS probable membrane antigen P140 (tegument protein).

GN BNRFL1
OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
OC viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus;
OX NCBI_TAXID:10377;
RN [1]
RP COMPLETE GENOME.
RX MEDLINE:84276667; PubMed:6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnall P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RN Nature 310:207-211(1984).
RN [2]
RP SEQUENCE FROM N. A.
RX MEDLINE:8604599; PubMed:2998073;
RA Hudson G.S., Bankier A.T., Satchwell S.C., Barrell B.G.;
RT "The short unique region of the B95-8 Epstein-Barr virus genome.";
RL Virology 147:81-98(1985).
CC -!- FUNCTION: tegument protein.
-!- SIMILARITY: TO BOTH 140 kDa MEMBRANE ANTIGEN ENCODED AT THE
EXTREMITIES OF THE HERPESVIRUS SAIMIRI GENOME (3 AND 75/EILP1).
CC
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CC
DR EMBL; V01555; CRA24862.1;
DR EMBL; M11924; AAA45899.1;
DR PIR; A03740; Q0071;
DR InterPro; IPR000728; AIRS-related.
DR Pfam; PF02769; AIRS_C; 1.
KW Membrane; Antigen; Late protein; Structural protein.
SQ SEQUENCE 1318 AA; 142843 MW; 58D1DC644EB84BE6_CRC64;
Query Match 43.8%; Score 7; DB 1; Length 1318;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 ARAAARR 11
DB 322 ARAAARR 328

Search completed: August 9, 2003, 16:29:52
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